

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Huston, James S.  
Houston, L. L.  
Ring, David B.  
Oppermann, Hermann

(ii) TITLE OF INVENTION: Biosynthetic Binding Proteins For  
Imaging

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department  
(B) STREET: Exchange Place, 53 State Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kelley, Robin D.  
(B) REGISTRATION NUMBER: 34,637  
(C) REFERENCE/DOCKET NUMBER: 2054/22

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..752

(D) OTHER INFORMATION: /product= "741F8 sFv' C-terminal Gly4-Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CC ATG GCG GAG ATC CAA TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG	47
Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys	
1 5 10 15	
CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ACC TTC	95
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
20 25 30	
ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA	143
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
AAG TGG ATG GGC TGG ATA AAC ACC AAC ACT GGA GAG CCA ACA TAT GCT	191
Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala	
50 55 60	
GAA GAG TTC AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC AGC	239
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser	
65 70 75	
ACT GCC TAT TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC ACG GCT ACA	287
Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr	
80 85 90 95	
TAT TTC TGT GGA AGG CAA TTT ATT ACC TAC GGC GGG TTT GCT AAC TGG	335
Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp	
100 105 110	
GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA TCG AGC TCC TCC GGA TCT	383
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser	
115 120 125	
TCA TCT AGC GGT TCC AGC TCG AGC GAT ATC GTC ATG ACC CAG TCT CCT	431
Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro	
130 135 140	
AAA TTC ATG TCC ACG TCA GTG GGA GAC AGG GTC AGC ATC TCC TGC AAG	479
Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys	
145 150 155	

GCC AGT CAG GAT GTG AGT ACT GCT GTA GCC TGG TAT CAA CAA AAA CCA	527
Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro	
160 165 170 175	
GGA GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TAT ACT	623
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr	
195 200 205	
CTC ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA CTT CAT TAC TGT	671
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys	
210 215 220	
CAG CAA CAT TAT AGA GTG CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG	719
Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu	
225 230 235	
GAG ATA AAA CGG GCT GAT GGG GGA GGT GGA TGT TAACGGGGGA GGTGGATGTT	772
Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys	
240 245 250	
GGGTCTCGTT ACGTTGCGGA TCTCGAGGCT ATCTTTACTA ACTCTTACCG TAAAGTTCTG	832
GCTCAACTGT CTGCACGCAA GCTTTTGCAG GATATCATGA GCGCTTAAGA TCCGTCGACC	892
TGCAGGCATG CAAGCTT	909

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro
1				5					10					15	
Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
			20					25					30		
Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys
		35					40					45			

Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu  
 50 55 60  
 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr  
 65 70 75 80  
 Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr  
 85 90 95  
 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser  
 115 120 125  
 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys  
 130 135 140  
 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala  
 145 150 155 160  
 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly  
 165 170 175  
 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly  
 180 185 190  
 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu  
 195 200 205  
 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln  
 210 215 220  
 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu  
 225 230 235 240  
 Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys  
 245 250

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 779 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..758

(D) OTHER INFORMATION: /product= "26-10 sFv" with  
C-terminal Gly4-Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CC ATG GAA GTT CAA CTG CAA CAG TCT GGT CCT GAA TTG GTT AAA CCT	47
Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro	
1 5 10 15	
GGC GCC TCT GTG CGC ATG TCC TGC AAA TCC TCT GGG TAC ATT TTC ACC	95
Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr	
20 25 30	
GAC TTC TAC ATG AAT TGG GTT CGC CAG TCT CAT GGT AAG TCT CTA GAC	143
Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp	
35 40 45	
TAC ATC GGG TAC ATT TCC CCA TAC TCT GGG GTT ACC GGC TAC AAC CAG	191
Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln	
50 55 60	
AAG TTT AAA GGT AAG GCG ACC CTT ACT GTC GAC AAA TCT TCC TCA ACT	239
Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr	
65 70 75	
GCT TAC ATG GAG CTG CGT TCT TTG ACC TCT GAG GAC TCC GCG GTA TAC	287
Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr	
80 85 90 95	
TAT TGC GCG GGC TCC TCT GGT AAC AAA TGG GCC ATG GAT TAT TGG GGT	335
Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly	
100 105 110	
CAT GGT GCT AGC GTT ACT GTG AGC TCC TCC GGA TCT TCA TCT AGC GGT	383
His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly	
115 120 125	
TCC AGC TCG AGT GGA TCC GAC GTC GTA ATG ACC CAG ACT CCG CTG TCT	431
Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser	
130 135 140	
CTG CCG GTT TCT CTG GGT GAC CAG GCT TCT ATT TCT TGC CGC TCT TCC	479
Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser	
145 150 155	
CAG TCT CTG GTC CAT TCT AAT GGT AAC ACT TAC CTG AAC TGG TAC CTG	527
Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu	
160 165 170 175	

CAA AAG GCT GGT CAG TCT CCG AAG CTT CTG ATC TAC AAA GTC TCT AAC	575
Gln Lys Ala Gly Gln Ser Pro Lys Leu Ile Tyr Lys Val Ser Asn	
180 185 190	
CGC TTC TCT GGT GTC CCG GAT CGT TTC TCT GGT TCT GGT TCT GGT ACT	623
Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr	
195 200 205	
GAC TTC ACC CTG AAG ATC TCT CGT GTC GAG GCC GAA GAC CTG GGT ATC	671
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile	
210 215 220	
TAC TTC TGC TCT CAG ACT ACT CAT GTA CCG CCG ACT TTT GGT GGT GGC	719
Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly	
225 230 235	
ACC AAG CTC GAG ATT AAA CGT TCC GGG GGA GGT GGA TGT TAACTGCAGC	768
Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Cys	
240 245 250	
CCGGGGGATC C	779

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly	
1 5 10 15	
Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp	
20 25 30	
Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr	
35 40 45	
Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys	
50 55 60	
Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala	
65 70 75 80	
Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr	
85 90 95	

Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His  
 100 105 110  
 Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser  
 115 120 125  
 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu  
 130 135 140  
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 145 150 155 160  
 Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln  
 165 170 175  
 Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg  
 180 185 190  
 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 195 200 205  
 Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr  
 210 215 220  
 Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr  
 225 230 235 240  
 Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys  
 245 250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: /product= "520C9 sFv polypeptide sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAG ATC CAA TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG CCT GGA GAG Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 1 5 10 15	48
ACA GTC AAG ATC TCC TGC AAG GCT TCT GGA TAT ACC TTC GCA AAC TAT Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr 20 25 30	96
GGA ATG AAC TGG ATG AAG CAG GCT CCA GGA AAG GGT TTA AAG TGG ATG Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 35 40 45	144
GGC TGG ATA AAC ACC TAC ACT GGA CAG TCA ACA TAT GCT GAT GAC TTC Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe 50 55 60	192
AAG GAA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC ACC ACT GCC CAT Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His 65 70 75 80	240
TTG CAG ATC AAC AAC CTC AGA AAT GAG GAC TCG GCC ACA TAT TTC TGT Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys 85 90 95	288
GCA AGA CGA TTT GGG TTT GCT TAC TGG GGC CAA GGG ACT CTG GTC AGT Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser 100 105 110	336
GTC TCT GCA TCG ATA TCG AGC TCC TCC GGA TCT TCA TCT AGC GGT TCC Val Ser Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Ser Gly Ser 115 120 125	384
AGC TCG AGT GGA TCC GAT ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu 130 135 140	432
TCT GCC TCT CTG GGA GAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln 145 150 155 160	480
GAC ATT GGT AAT AGC TTA ACC TGG CTT CAG CAG GAA CCA GAT GGA ACT Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr 165 170 175	528
ATT AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GAT TCT GGT GTC CCC Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro 180 185 190	576



AAA AGG TTC AGT GGC AGT CGG TCT GGG TCA GAT TAT TCT CTC ACC ATC	624
Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile	
195 200 205	
AGT AGC CTT GAG TCT GAA GAT TTT GTA GTC TAT TAC TGT CTA CAA TAT	672
Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr	
210 215 220	
GCT ATT TTT CCG TAC ACG TTC GGA GGG GGG ACC AAC CTG GAA ATA AAA	720
Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys	
225 230 235 240	
CGG GCT GAT TAATCTGCAG	739
Arg Ala Asp	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu	15
1 5 10	
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr	30
20 25	
Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met	45
35 40	
Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe	60
50 55	
Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His	80
65 70 75	
Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys	95
85 90	
Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser	110
100 105	
Val Ser Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser	125
115 120	

Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
 130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln  
 145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr  
 165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro  
 180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile  
 195 200 205

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr  
 210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys  
 225 230 235 240

Arg Ala Asp

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
- (A) NAME/KEY: Protein
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "Linker 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "LINKER 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly  
1                      5                                      10                                      15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Cys  
1

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "C-Terminal Tail  
(Gly-Gly-Gly-Gly-Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Gly Gly Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "C-Terminal Tail  
(His-His-His-His-His-His-Gly-Gly-Gly-Gly-Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His His His His His His Gly Gly Gly Gly Cys  
1 5 10